

CCT	CCG	COC	COT	CYA	GAQ	GGC	CTY	CTG	GAC	AGC	GGC	CTC	ATC	TTG	AGG	CAC	AGA	CGC	GTG	AAC	GAC	CAA
CCG	CTC	TCT	CTA	ACT	GGG	GAG	GGG	GGC	AGC	AGC	GGC	AGC	ACT	TTT	CAG	TTG	TCC	CGC	GTG	AGC	GAA	
CAG	CAC	CAT	CTG	CTT	GGG	AGA	ACC	CTC	TCC	CTT	CTC	TGA	GAA	AGA	AAG	ATG	TGC	ATG	TGG	ATC	GGG	
TAT	TCC	AGA	GA'	AA'	AA'	AA'	AA'	AA'	AA'	AA'	AA'	AA'	AA'	AA'	AA'	AA'	AA'	AA'	AA'	AA'	AA'	
T	B	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	
CCG	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	CTC	
Y	I	Q	V	E	P	V	L	D	Y	L	T	L	L	P	A	E	V	E	F	E	E	
CAG	ATT	CAG	AGG	ACA	CTG	ACC	ACC	TTC	GGG	AAC	ATG	CAG	GCA	GTG	GAA	CTG	CTG	CTG	AGC	CTG	AGC	
CTG	TTG	Q	R	T	V	A	C	T	S	G	H	M	Q	A	V	E	G	L	L	C	T	
ACC	TTG	QAG	AGG	AGA	CTG	TGG	CAC	CTT	GGT	TGG	ACT	COG	GAA	TTC	GTG	GAG	GCC	CTC	CGG	CTC	CGG	
L	E	K	G	V	H	B	H	B	H	B	H	B	H	B	H	B	H	B	H	B	H	
AGA	ATT	GAG	AGA	AGA	CTG	AGG	CTG	AGG	CTG	AGG	CTG	AGG	CTG	AGG	CTG	AGG	CTG	AGG	CTG	AGG	CTG	
R	T	O	S	P	L	A	A	A	R	Y	H	E	E	E	E	E	E	E	E	E	E	
CCA	TGG	TTT	GAG	AGC	GCT	CAT	GAT	GAA	TAT	CTC	CAG	ATG	CTG	AAC	CTC	CTT	GAG	CC	ACT	CT	ACT	
S	P	F	E	B	A	H	D	E	Y	L	Q	L	L	L	L	L	L	L	L	L	L	
CTG	OTG	QAC	AGG	CTT	CTA	OTG	AGA	GAG	OTC	TTG	GAT	ABG	TCG	ATG	AGG	GAG	GAA	CTG	TTG	TTG	TTG	
L	V	D	K	L	R	L	R	D	V	L	D	Y	L	D	Y	L	D	Y	L	D	Y	
AGA	ATT	GAG	AGA	AGA	CTG	AGG	CTG	AGG	CTG	AGG	CTG	AGG	CTG	AGG	CTG	AGG	CTG	AGG	CTG	AGG	CTG	
E	T	O	R	A	B	R	A	B	R	A	B	R	A	B	R	A	B	R	A	B	R	
AGA	GAG	CTA	AGA	AAA	AGG	ATT	OTG	CAG	AGG	AGG	AAC	TGG	TTG	CTG	CTG	CTG	CTG	CTG	CTG	CTG	CTG	
R	E	L	L	K	R	I	V	Q	K	E	#	#	#	#	#	#	#	#	#	#	#	
CTT	CGT	CAA	ACA	AGA	AAC	AAT	GAA	CTT	CTC	CAG	AGG	TTA	ACA	GGC	TCT	GAT	TGC	TCA	GAA	CTT	GAA	
L	R	Q	T	G	H	E	H	E	L	V	Q	E	L	T	C	S	D	C	C	C	C	
S	#	A	E	I	E	H	L	TA	CA	C	A	S	Q	V	D	Q	P	Q	V	E	Q	
CTT	CA	ACC	ACA	GTG	CAG	CA	AAT	CTG	GAG	AGG	GAG	OTC	TGG	GGC	ATG	GAG	AAT	ACA	TCA	CTA	CTA	
L	S	T	T	V	Q	P	H	L	E	K	E	V	W	Q	H	G	#	#	#	#	#	
TCA	GAA	TCA	TCT	TTT	GCA	GAT	TCT	TCT	GTG	ATT	TCA	GAA	TCG	ACA	AGT	TTG	CGA	GAA	S	GAA	S	
S	GA	S	B	F	A	D	S	S	V	V	S	V	S	V	S	V	S	V	S	V	S	
G	S	V	S	C	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	
GGC	ACC	ATG	GGG	AGT	TCA	GAT	TCA	GAT	GAA	GAG	CTG	GGC	AGA	AGA	AGA	TCC	CCG	GAG	TCA	CTA	CTA	
G	T	N	G	D	S	C	D	A	E	H	V	A										

CATTGAACTC TTTTAAAGAA CACAATATAT TANGCATTAT CCATCTTATT
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H-2      -MAEGNHRKKKPLKVLKSLGKDFLTGVLDNLVEQNVLNWKKEKKYFYD-AKTEDKVEVMA 58
E        -MADKVLKPKKKLFIKSMGEGTINGLLDELLQTEVLNKEEMKVKPEN-ATVMDKTRALI 58
P1-453   -ASDDLSLIRFNFMALEFQQLTCVLPILDNLKFNVINFEHDIIVQV--TQISLQAFELI 58
P2-439   -ESNDLLIRFNRMALEFQHLTCVLPILDNLKFNVINFEHDIIVQV--TQISLQAFELI 57
H-1      -AHPHHQETLFFNRVVLAKQLLSELEHLELDITTEMSLEIQAF--VGSFSONVELL 57
a5-125   -----LVDKLLVSDVLDKCEEEELTIEDFNPIAAAENNGNESGVPELL 44
IDD      -EARDKQVLSLPLLELGAEVLVEGLVQYLYQEGILTENHQBINAQ--TTGLRRTMILL 58
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H-2      DSMQEFQRMAGQMLLQTFPNIDQISP-----NKKAHPNMEAGPPESGESTDALKLCPHE 112
E        DSVIEFGAQACQICITYICEEDSYLAGTIGLSAAPQAVQDNPAAMPTSSGSEGNVKLCSLE 118
P1-453   DTILVEGNAAANIFKNCLKEIDSTLY-----NLEVDKNNKYYIP----TEDVSGLSLEE 108
P2-439   DTILVEGNIAATVPRNSLQBAEAVLY-----EHLFVQQDIKYIP----TEDVSDLPVEE 107
H-1      NLLPFFGPGQAFDAFCEALRETKQGHLED--KLLTTISGLQHVLRPLSCDYDLSLPPPVCE 115
a5-125   -EIVQK----- 50
IDD      DILFSGPKAFDTFLDSLQEFPPWVEK-----KFAPEEAMTDLP----AGDPLTGIPSH 109
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F4A1 -----MSASQDSFSDNGP----- 14
 8RNAhelicase -----MSGYSSDRDFGRDPGFGAZPFGG----- 23
 a-5 -----MLSTLEKGVVHLGWTRFVFEALRFTGSPLAAPYMNFEELTDLSPSPFENAHDEYLLQLNL 120

F4A1 -----DGME-----EGVIESNWN-- 28
 8RNAhelicase -----SPAGPLSGYFPGNP-----GEKLVKKKWNLD 49
 a-5 -----QETLVKLLVFDVLDKCMEEELLTIEDPNKIAAAENNGNESGVFEELKPIWQENWPSA 180

F4A1 -----EL-----EFYFNFYQEHPLARPTAQEVETYPFSKEITVPGH 87
 8RNAhelicase -----EL-----EFYFNFYQEHPLARPTAQEVETYPFSKEITVPGH 87
 a-5 -----ELNVLRTQGNNEIVQELTGSDCSESNAEIEENLSQVDGFPQVEEQLLSTTVQPNLEKEVWGM 240

F4A1 -----EIVDSFDDMNL-----ESLLRGIYAYG 51
 8RNAhelicase -----NCFKPVLFNFIYANFP-----ANVMDVIAPQN 113
 a-5 -----ENNSSESPADSSVVSSESDTSLAEGSVSCLDES LGHNSNMGSDSGTMGSDSDEENVAARA 300

F4A1 -----EHP-----SAIQORAILPCINGYDVIAQAQSGTGKTATFAISILQQIELD-----EKATQ 102
 8RNAhelicase -----EHP-----TAIQAQGWVPVALSGLDMVGVAQTGSGKTLSYLLPAIVHINHPFLERGDGP 169
 a-5 -----SPEBELQLRPYQMEVAQPALEBGNIIICLTGSGYTPVAVYIAKDHLDKYK-----KASEPGK 358

F4A1 -----ELVLAPTRRLAQIQ----- 117
 8RNAhelicase -----ELVLAPTRRLAQIQ----- 184
 a-5 -----ELVLVKNVLLVQLPFRKEFPQFLYFWYPVIGLSGDTQLKISFPEVVKSCDIISTAQILE 418

F4A1 -----KV 120
 8RNAhelicase -----QVA 187
 a-5 -----NSLLNLENGEDAGVQLSDPSLIIDECCHTNKEAVYNNIMPHYLMQKLNRLKKNKPKV 478

F4A1 -----MALGDYMGASCHACIGGTNVRAEVQKLQMEAPHIIVGTPGRVFDMLNRRYLSPKYIEMFV 180
 8RNAhelicase -----AEYCRACRLKSTCIYGGAPKGPQIRDLEGR-VEICIAATPGRLIDFLECGKTNLRRTTYLV 246
 a-5 -----ELPLQILGLTASPGVGATKQAKAEHILKLCANLDAPTITKTVKENLDQLKNQIQEPCKK 538

F4A1 -----LDEADEMLSRGPKDQIYDIFQKLNSTQVLLSATMPSDVLEVTKKFRDPPIRILVKKKE 240
 8RNAhelicase -----LDEADRMMLDMGFEPQIRKIVDQIRPDROTLMWSATWPKEVRQLAEDFLKDYIHINIGALE 306
 a-5 -----EAIADATREDPFKEKLEIMTRIQTQYQMSPHSDPFGTQPYEQWAIQMEKKAACKGNRKE 598

F4A1 -----LLEGIRQP-----YINVEREKKWLDLTLCD--- 265
 8RNAhelicase -----LSANHNILQ-----IVDVCHDVEKDEKLIR--- 331
 a-5 -----VCAEHLRKYNALQINDTIFMIDAYTHLETYPYNEEKDEKPAVIDEDDSDEGGDDEYCDGDE 658

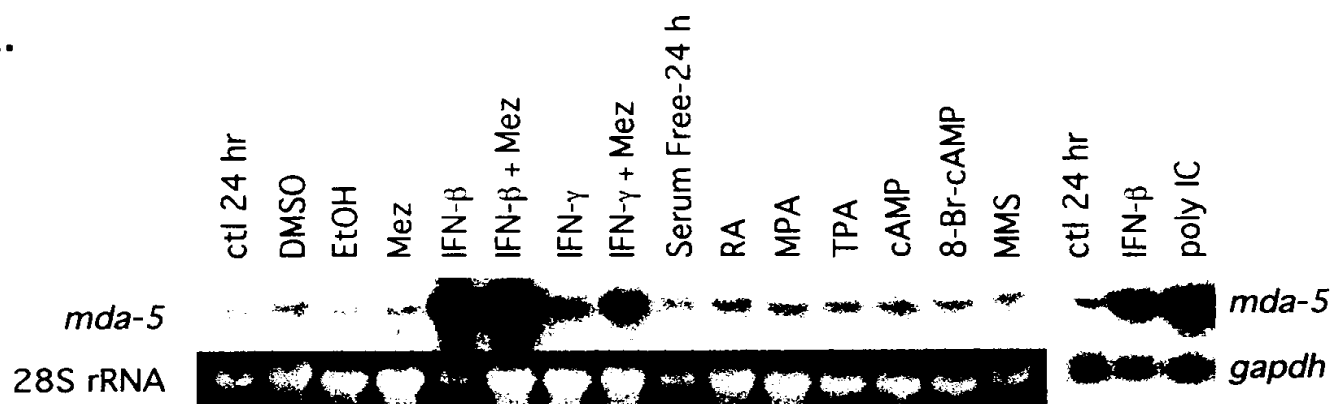
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 a-5 -----DEDDLKKPLKLDDETRPLMTLFFENNMKLKPLAENPEYENEKLTKLRLTIMEQYTRTES 718

F4A1 -----QAVIFINTER-----KVDWLTEKMHAFDFTVSAHGD-----MDQKERVIMREF 318
 8RNAhelicase -----NKTIVFVETKR-----RCDELTPKMPHDGWPAMGIHGD-----SQQEPDWVLNEF 387
 a-5 -----REGIIFTTTPQAYALSQWITENEKFAEVGVFAHHLGAGHSSEFPYPMQTONEQFEVISKF 778

F4A1 -----SGSSRVLLITDLLARGIDVQVSVLEVINYDLPTNRENYIHRIGRG-----GRFGKGV 371
 8RNAhelicase -----MHGKAPILIATDVASRGLDVEDVKEVINYDYPNSSEDIHRIGRT-----APSTKTGT 440
 a-5 -----TGKINLLIATTVAEGLDIECNIVIRYGLVTNEIAMVQARGRARADESTYVLVAHSGS 838

F4A1 -----VINMVTEEDKPTLRDIETFYNTSIEEMPLNVADLI----- 406
 8RNAhelicase -----LYTFPTPNNIKQVSDLSVLSBANQAINPFLQLVEDFGSGPSRGGGMDDEPDYSAG 500
 a-5 -----GVIEHETVNDPEKMYKACHVQNMKEEYAHKILELQMSIEEYKMYKTYRNIAKHYN 898

A.



B.

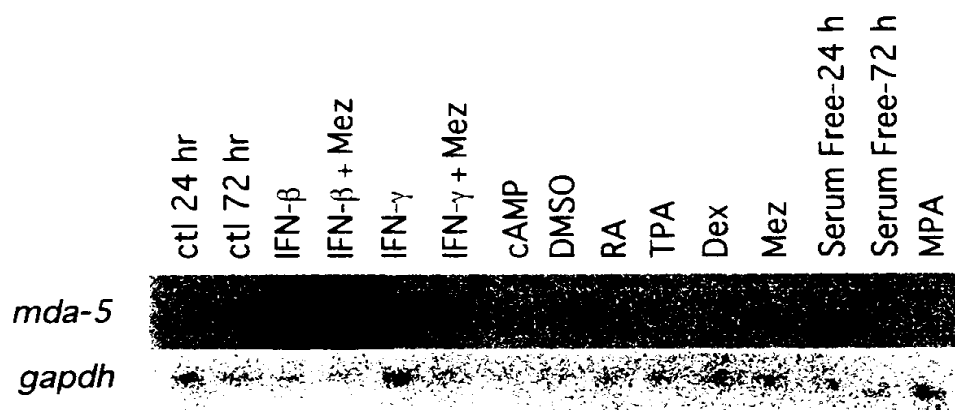
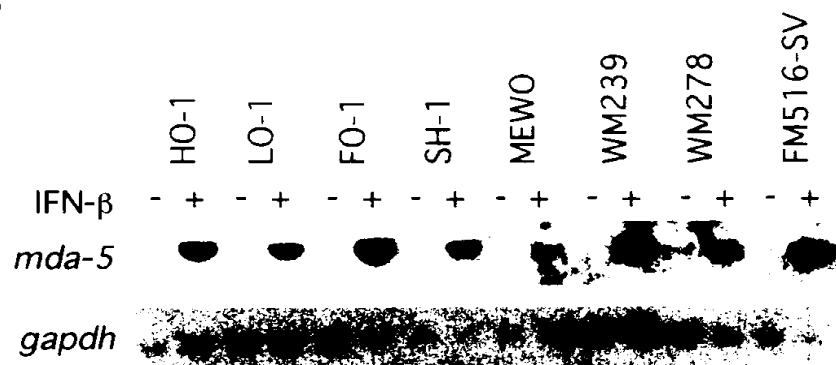


Figure 2

A.



B.

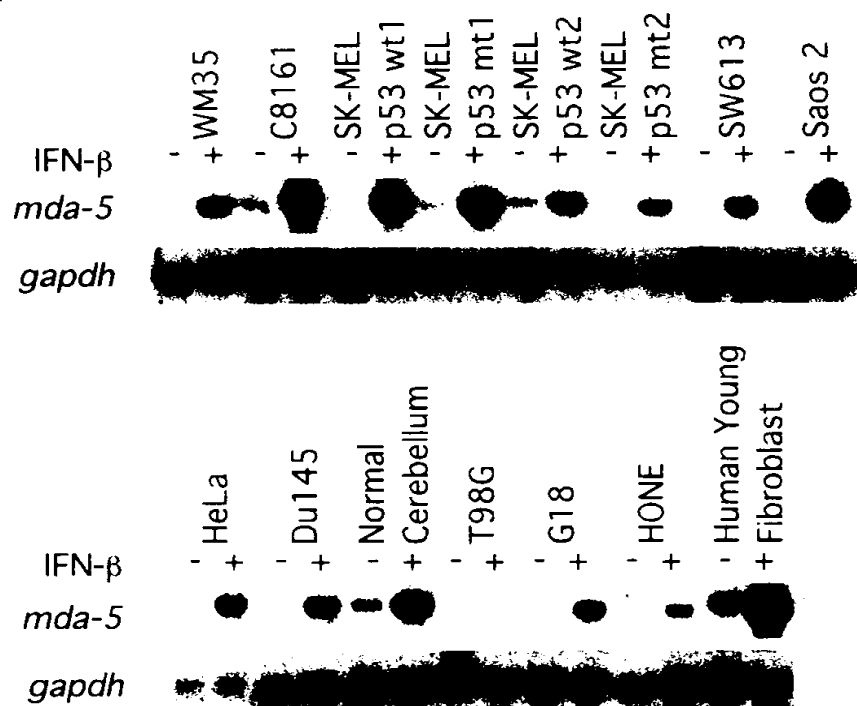
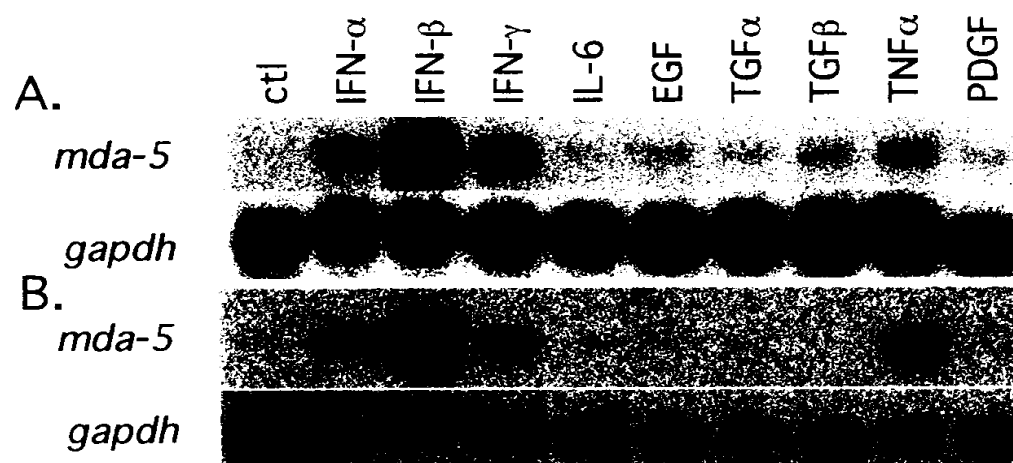


Figure 3



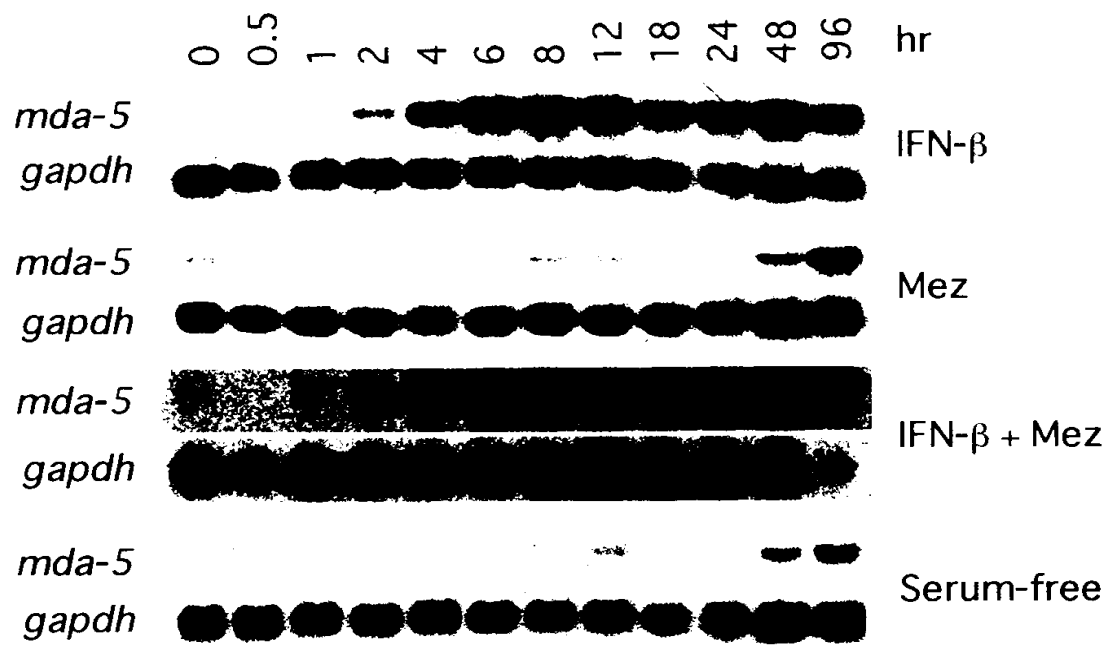


Figure 5

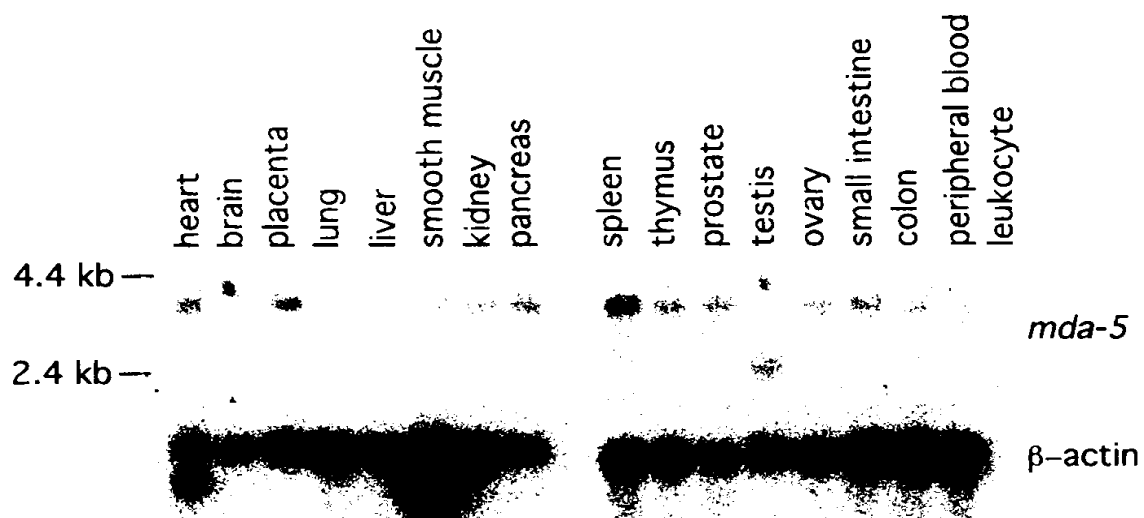
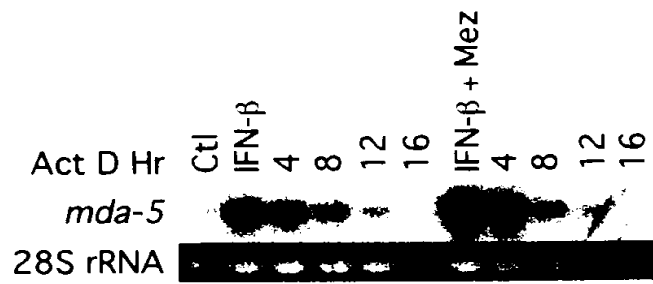
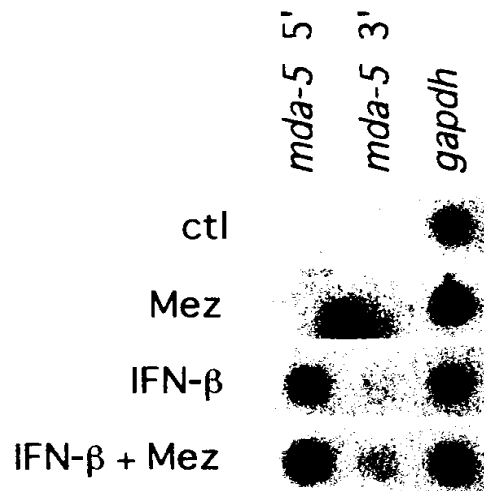


Figure 6

A.



B.



C.

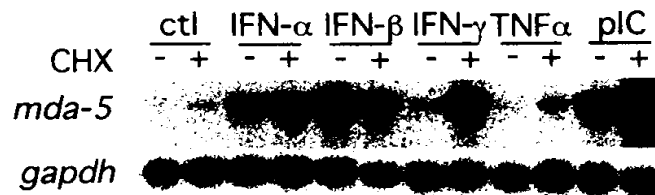
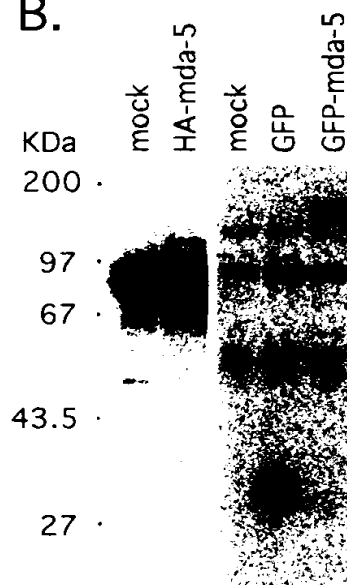


Figure 7

A.



B.



C.

